

10/560760

43

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SEQUENCE LISTING

<110> Evologic S.A.

Maliere Technologies Société Civile

Rhodia Chimie

Marliere, Phillipe

<120> Cloning of gluconate dehydratase gcnD gene

<130> G 3111 EP

<160> 33

<170> PatentIn version 3.1

<210> 1

<211> 1812

<212> DNA

<213> Agrobacterium tumefaciens

<220>

<221> CDS

<222> (1)..(1809)

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ctc gag cgt tac atg aac ttc ggt ctc agc cag gcc gag ctt cag tcc	144
Leu Glu Arg Tyr Met Asn Phe Gly Leu Ser Gln Ala Glu Leu Gln Ser	
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<211> 603

<212> PRT

<213> Agrobacterium tumefaciens

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 35 40 45

 Asp Arg Pro Ile Ile Gly Ile Ala Gln Thr Gly Ser Asp Leu Ser Pro
 50 55 60

 Cys Asn Arg His His Leu Glu Leu Ala Asn Arg Leu Arg Glu Gly Ile
 65 70 75 80

 Arg Glu Ala Gly Gly Ile Ala Ile Glu Phe Pro Val His Pro Ile Gln
 85 90 95

 Glu Thr Gly Lys Arg Pro Thr Ala Gly Leu Asp Arg Asn Leu Ala Tyr
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Leu Gly Leu Val Glu Val Leu Tyr Gly Tyr Pro Leu Asp Gly Val Val
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Leu Thr Ile Gly Cys Asp Lys Thr Thr Pro Ala Cys Leu Met Ala Ala
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Ala Thr Val Asn Ile Pro Ala Ile Ala Leu Ser Val Gly Pro Met Leu
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Asn Gly Trp Phe Arg Gly Glu Arg Thr Gly Ser Gly Thr Ile Val Trp
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Lys Ala Arg Glu Leu Leu Ala Lys Gly Glu Ile Asp Tyr Gln Gly Phe
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Val Lys Leu Val Ala Ser Ser Ala Pro Ser Thr Gly Tyr Cys Asn Thr
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Met Gly Thr Ala Thr Thr Met Asn Ser Leu Ala Glu Ala Leu Gly Met
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Gln Leu Pro Gly Ser Ala Ala Ile Pro Ala Pro Tyr Arg Asp Arg Gln
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Glu Val Ser Tyr Leu Thr Gly Leu Arg Ile Val Asp Met Val Arg Glu
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Asp Leu Lys Pro Ser Asp Ile Met Thr Lys Asp Ala Phe Ile Asn Ala
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Leu Asn Gly Leu Ala Arg His Val Gly Val Glu Leu Thr Val Asp Asp
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 385 390 395 400

Met Lys Thr Ser Val Ile Ser Glu Glu Phe Arg Gly Arg Tyr Leu Ser
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Gly Pro Glu Asp Tyr His His Arg Ile Asp Asp Pro Ser Leu Gly Ile
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Asp Ala Asn Thr Val Leu Phe Met Arg Gly Ala Gly Pro Ile Gly Tyr
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 515 520 525

Asp Val Gly Arg Gly Lys Ala Asp Ile Leu Ile Ser Gly Glu Glu Leu
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Asp His Gln Thr Pro Trp Gln Glu Ile Gln Arg Gly Ile Val Ser Gln
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35 40 45	
cgg gat cgc ttt ctt gcg ctt gtc tcg gcc cat gga gcg aag gcg gct	192
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Pro His Ala Lys Thr Pro Met Cys Pro Glu Ile Ala Ile Asp Leu Ile	
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Glu Ala Gly Ala Trp Gly Ala Thr Val Ala Asp Leu Phe Gln Ala Glu	
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Val Leu Leu Lys Ala Gly Val Ser Asn Ile Leu Ile Ala Asn Gln Ile	
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ggc gga ttg aca tcc gcc aga cgc cta cgc atg ctc gca gat gct ttt	384
Gly Gly Leu Thr Ser Ala Arg Arg Leu Arg Met Leu Ala Asp Ala Phe	
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gca aag gat atc atc gac acc atc tcg aca agt gca gaa atc gta ctg Ala Lys Asp Ile Ile Asp Thr Ile Ser Thr Ser Ala Glu Ile Val Leu 180 185 190			576
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 385 390 395 400

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 Arg Asp Arg Phe Leu Ala Leu Val Ser Ala His Gly Ala Lys Ala Ala
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 Pro His Ala Lys Thr Pro Met Cys Pro Glu Ile Ala Ile Asp Leu Ile
 65 70 75 80

 Glu Ala Gly Ala Trp Gly Ala Thr Val Ala Asp Leu Phe Gln Ala Glu
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 Val Leu Leu Lys Ala Gly Val Ser Asn Ile Leu Ile Ala Asn Gln Ile
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 Gly Gly Leu Thr Ser Ala Arg Arg Leu Arg Met Leu Ala Asp Ala Phe
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 Pro Lys Ala Glu Ile Ile Cys Cys Val Asp Ser Val Gln Ala Ser Ala

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Phe Ile Glu Val Gly Val Gly Arg Thr Gly Ala Arg Thr Leu Asn Val				
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Ala Lys Asp Ile Ile Asp Thr Ile Ser Thr Ser Ala Glu Ile Val Leu				
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Ala Gly Val Ser Thr Tyr Glu Gly Ser Val Ser Gly Glu Thr Ser Glu				
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Ala Leu Asp Ala Asn Met Ala Ala Leu Phe Asp Leu Leu Thr Asp Ser				
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Leu Ala Ser Ile Arg Glu Lys Asp Pro Gly Arg Pro Leu Thr Val Ser				
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Ala Gly Gly Ser Ile His Phe Asp Arg Val Leu Ala Ala Leu Val Pro				
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Val Cys Glu Ala Asp Gly Asn Ala Thr Leu Leu Leu Arg Ser Gly Ala				
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Ile Phe Phe Ser Asp His Gly Val Tyr Gln Arg Gly Phe Gln Ala Val				
	275		280	285
Asp Ala Arg Asn Leu Leu Ala Ser Gly Lys Val Val Phe Lys Ala Ser				
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Glu Ala Phe Gln Pro Ser Met Arg Ile Trp Ala Glu Val Ile Ser Val				
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Pro Glu Pro Gly Leu Ala Ile Val Gly Met Gly Met Arg Asp Val Ser				
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Phe Asp Gln Asp Leu Pro Val Ala Leu Arg Leu His Arg Asp Gly His				
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Leu Val Glu Ala Asp Leu Ser Ser Ser Ala Lys Val Gly Lys Leu Asn				
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370

375

380

Gly Asp Val Ile Glu Phe Gly Ile Ser His Pro Cys Thr Cys Phe Asp
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<213> artificial sequence

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<212> DNA

<213> vector

<400> 15

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actcctgttg atagatccag taatgacctc agaactceat ctggatttgt tcagaacgct 240
cggttgccgc cgggcgtttt ttattggtga gaatccaagc tagcttggcg agattttcag 300

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<211> 30

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 16

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<210> 17

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<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 17

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30

<210> 18

<211> 1707

<212> DNA

<213> Zymomonas mobilis

<220>

<221> CDS

<222> (1)..(1707)

<223>

<400> 18

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Met Ser Tyr Thr Val Gly Thr Tyr Leu Ala Glu Arg Leu Val Gln Ile
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48

ggt ctc aag cat cac ttc gca gtc gcg ggc gac tac aac ctc gtc ctt
Gly Leu Lys His His Phe Ala Val Ala Gly Asp Tyr Asn Leu Val Leu
20 25 30

96

ctt gac aac ctg ctt ttg aac aaa aac atg gag cag gtt tat tgc tgt
Leu Asp Asn Leu Leu Leu Asn Lys Asn Met Glu Gln Val Tyr Cys Cys
35 40 45

144

aac gaa ctg aac tgc ggt ttc agt gca gaa ggt tat gct cgt gcc aaa
Asn Glu Leu Asn Cys Gly Phe Ser Ala Glu Gly Tyr Ala Arg Ala Lys
50 55 60

192

ggc gca gca gca gcc gtc gtt acc tac agc gtc ggt gcg ctt tcc gca Gly Ala Ala Ala Ala Val Val Thr Tyr Ser Val Gly Ala Leu Ser Ala 65 70 75 80	240
ttt gat gct atc ggt ggc gcc tat gca gaa aac ctt ccg gtt atc ctg Phe Asp Ala Ile Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu 85 90 95	288
atc tcc ggt gct ccg aac aac aat gat cac gct gct ggt cac gtg ttg Ile Ser Gly Ala Pro Asn Asn Asn Asp His Ala Ala Gly His Val Leu 100 105 110	336
cat cac gct ctt ggc aaa acc gac tat cac tat cag ttg gaa atg gcc His His Ala Leu Gly Lys Thr Asp Tyr His Tyr Gln Leu Glu Met Ala 115 120 125	384
aag aac atc acg gcc gcc gct gaa gcg att tac acc ccg gaa gaa gct Lys Asn Ile Thr Ala Ala Ala Glu Ala Ile Tyr Thr Pro Glu Glu Ala 130 135 140	432
ccg gct aaa atc gat cac gtg att aaa act gct ctt cgt gag aag aag Pro Ala Lys Ile Asp His Val Ile Lys Thr Ala Leu Arg Glu Lys Lys 145 150 155 160	480
ccg gtt tat ctc gaa atc gct tgc aac att gct tcc atg ccc tgc gcc Pro Val Tyr Leu Glu Ile Ala Cys Asn Ile Ala Ser Met Pro Cys Ala 165 170 175	528
gct cct gga ccg gca agc gca ttg ttc aat gac gaa gcc agc gac gaa Ala Pro Gly Pro Ala Ser Ala Leu Phe Asn Asp Glu Ala Ser Asp Glu 180 185 190	576
gct tct ttg aat gca gcg gtt gaa gaa acc ctg aaa ttc atc gcc aac Ala Ser Leu Asn Ala Ala Val Glu Glu Thr Leu Lys Phe Ile Ala Asn 195 200 205	624
cgc gac aaa gtt gcc gtc ctc gtc ggc agc aag ctg cgc gca gct ggt Arg Asp Lys Val Ala Val Leu Val Gly Ser Lys Leu Arg Ala Ala Gly 210 215 220	672
gct gaa gaa gct gct gtc aaa ttt gct gat gct ctc ggt ggc gca gtt Ala Glu Glu Ala Ala Val Lys Phe Ala Asp Ala Leu Gly Gly Ala Val 225 230 235 240	720
gct acc atg gct gct gca aaa agc ttc ttc cca gaa gaa aac ccg cat Ala Thr Met Ala Ala Ala Lys Ser Phe Phe Pro Glu Glu Asn Pro His 245 250 255	768
tac atc ggc acc tca tgg ggt gaa gtc agc tat ccg ggc gtt gaa aag Tyr Ile Gly Thr Ser Trp Gly Glu Val Ser Tyr Pro Gly Val Glu Lys 260 265 270	816
acg atg aaa gaa gcc gat gcg gtt atc gct ctg gct cct gtc ttc aac Thr Met Lys Glu Ala Asp Ala Val Ile Ala Leu Ala Pro Val Phe Asn 275 280 285	864
gac tac tcc acc act ggt tgg acg gat att cct gat cct aag aaa ctg Asp Tyr Ser Thr Thr Gly Trp Thr Asp Ile Pro Asp Pro Lys Lys Leu 290 295 300	912

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Val Leu Ala Glu Pro Arg Ser Val Val Val Asn Gly Ile Arg Phe Pro	
305 310 315 320	
agc gtc cat ctg aaa gac tat ctg acc cgt ttg gct cag aaa gtt tcc	1008
Ser Val His Leu Lys Asp Tyr Leu Thr Arg Leu Ala Gln Lys Val Ser	
325 330 335	
aag aaa acc ggt gca ttg gac ttc ttc aaa tcc ctc aat gca ggt gaa	1056
Lys Lys Thr Gly Ala Leu Asp Phe Phe Lys Ser Leu Asn Ala Gly Glu	
340 345 350	
ctg aag aaa gcc gct ccg gct gat ccg agt gct ccg ttg gtc aac gca	1104
Leu Lys Lys Ala Ala Pro Ala Asp Pro Ser Ala Pro Leu Val Asn Ala	
355 360 365	
gaa atc gcc cgt cag gtc gaa gct ctt ctg acc ccg aac acg acg gtt	1152
Glu Ile Ala Arg Gln Val Glu Ala Leu Leu Thr Pro Asn Thr Thr Val	
370 375 380	
att gct gaa acc ggt gac tct tgg ttc aat gct cag cgc atg aag ctc	1200
Ile Ala Glu Thr Gly Asp Ser Trp Phe Asn Ala Gln Arg Met Lys Leu	
385 390 395 400	
ccg aac ggt gct cgc gtt gaa tat gaa atg cag tgg ggt cac att ggt	1248
Pro Asn Gly Ala Arg Val Glu Tyr Glu Met Gln Trp Gly His Ile Gly	
405 410 415	
tgg tcc gtt cct gcc gcc ttc ggt tat gcc gtc ggt gct ccg gaa cgt	1296
Trp Ser Val Pro Ala Ala Phe Gly Tyr Ala Val Gly Ala Pro Glu Arg	
420 425 430	
cgc aac atc ctc atg gtt ggt gat ggt tcc ttc cag ctg acg gct cag	1344
Arg Asn Ile Leu Met Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln	
435 440 445	
gaa gtc gct cag atg gtt cgc ctg aaa ctg ccg gtt atc atc ttc ttg	1392
Glu Val Ala Gln Met Val Arg Leu Lys Leu Pro Val Ile Ile Phe Leu	
450 455 460	
atc aat aac tat ggt tac acc atc gaa gtt atg atc cat gat ggt ccg	1440
Ile Asn Asn Tyr Gly Tyr Thr Ile Glu Val Met Ile His Asp Gly Pro	
465 470 475 480	
tac aac aac atc aag aac tgg gat tat gcc ggt ctg atg gaa gtg ttc	1488
Tyr Asn Asn Ile Lys Asn Trp Asp Tyr Ala Gly Leu Met Glu Val Phe	
485 490 495	
aac ggt aac ggt ggt tat gac agc ggt gct ggt aaa ggc ctg aag gct	1536
Asn Gly Asn Gly Gly Tyr Asp Ser Gly Ala Gly Lys Gly Leu Lys Ala	
500 505 510	
aaa acc ggt ggc gaa ctg gca gaa gct atc aag gtt gct ctg gca aac	1584
Lys Thr Gly Gly Glu Leu Ala Glu Ala Ile Lys Val Ala Leu Ala Asn	
515 520 525	
acc gac ggc cca acc ctg atc gaa tgc ttc atc ggt cgt gaa gac tgc	1632
Thr Asp Gly Pro Thr Leu Ile Glu Cys Phe Ile Gly Arg Glu Asp Cys	
530 535 540	

act gaa gaa ttg gtc aaa tgg ggt aag cgc gtt gct gcc gcc aac agc 1680
 Thr Glu Glu Leu Val Lys Trp Gly Lys Arg Val Ala Ala Ala Asn Ser
 545 550 555 560

cgt aag cct gtt aac aag ctc ctc tag 1707
 Arg Lys Pro Val Asn Lys Leu Leu
 565

<210> 19

<211> 568

<212> PRT

<213> *Zymomonas mobilis*

<400> 19

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Gly Leu Lys His His Phe Ala Val Ala Gly Asp Tyr Asn Leu Val Leu
 20 25 30

Leu Asp Asn Leu Leu Leu Asn Lys Asn Met Glu Gln Val Tyr Cys Cys
 35 40 45

Asn Glu Leu Asn Cys Gly Phe Ser Ala Glu Gly Tyr Ala Arg Ala Lys
 50 55 60

Gly Ala Ala Ala Ala Val Val Thr Tyr Ser Val Gly Ala Leu Ser Ala
 65 70 75 80

Phe Asp Ala Ile Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu
 85 90 95

Ile Ser Gly Ala Pro Asn Asn Asn Asp His Ala Ala Gly His Val Leu
 100 105 110

His His Ala Leu Gly Lys Thr Asp Tyr His Tyr Gln Leu Glu Met Ala
 115 120 125

Lys Asn Ile Thr Ala Ala Ala Glu Ala Ile Tyr Thr Pro Glu Glu Ala
 130 135 140

Pro Ala Lys Ile Asp His Val Ile Lys Thr Ala Leu Arg Glu Lys Lys
 145 150 155 160

Pro Val Tyr Leu Glu Ile Ala Cys Asn Ile Ala Ser Met Pro Cys Ala
 165 170 175

Ala Pro Gly Pro Ala Ser Ala Leu Phe Asn Asp Glu Ala Ser Asp Glu
 180 185 190

Ala Ser Leu Asn Ala Ala Val Glu Glu Thr Leu Lys Phe Ile Ala Asn
 195 200 205

Arg Asp Lys Val Ala Val Leu Val Gly Ser Lys Leu Arg Ala Ala Gly
 210 215 220

Ala Glu Glu Ala Ala Val Lys Phe Ala Asp Ala Leu Gly Gly Ala Val
 225 230 235 240

Ala Thr Met Ala Ala Ala Lys Ser Phe Phe Pro Glu Glu Asn Pro His
 245 250 255

Tyr Ile Gly Thr Ser Trp Gly Glu Val Ser Tyr Pro Gly Val Glu Lys
 260 265 270

Thr Met Lys Glu Ala Asp Ala Val Ile Ala Leu Ala Pro Val Phe Asn
 275 280 285

Asp Tyr Ser Thr Thr Gly Trp Thr Asp Ile Pro Asp Pro Lys Lys Leu
 290 295 300

Val Leu Ala Glu Pro Arg Ser Val Val Val Asn Gly Ile Arg Phe Pro
 305 310 315 320

Ser Val His Leu Lys Asp Tyr Leu Thr Arg Leu Ala Gln Lys Val Ser
 325 330 335

Lys Lys Thr Gly Ala Leu Asp Phe Phe Lys Ser Leu Asn Ala Gly Glu
 340 345 350

Leu Lys Lys Ala Ala Pro Ala Asp Pro Ser Ala Pro Leu Val Asn Ala
 355 360 365

Glu Ile Ala Arg Gln Val Glu Ala Leu Leu Thr Pro Asn Thr Thr Val
 370 375 380

Ile Ala Glu Thr Gly Asp Ser Trp Phe Asn Ala Gln Arg Met Lys Leu
 385 390 395 400

Pro Asn Gly Ala Arg Val Glu Tyr Glu Met Gln Trp Gly His Ile Gly
 405 410 415

Trp Ser Val Pro Ala Ala Phe Gly Tyr Ala Val Gly Ala Pro Glu Arg
 420 425 430

Arg Asn Ile Leu Met Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln
 435 440 445

Glu Val Ala Gln Met Val Arg Leu Lys Leu Pro Val Ile Ile Phe Leu
 450 455 460

Ile Asn Asn Tyr Gly Tyr Thr Ile Glu Val Met Ile His Asp Gly Pro
 465 470 475 480

Tyr Asn Asn Ile Lys Asn Trp Asp Tyr Ala Gly Leu Met Glu Val Phe
 485 490 495

Asn Gly Asn Gly Gly Tyr Asp Ser Gly Ala Gly Lys Gly Leu Lys Ala
 500 505 510

Lys Thr Gly Gly Glu Leu Ala Glu Ala Ile Lys Val Ala Leu Ala Asn
 515 520 525

Thr Asp Gly Pro Thr Leu Ile Glu Cys Phe Ile Gly Arg Glu Asp Cys
 530 535 540

Thr Glu Glu Leu Val Lys Trp Gly Lys Arg Val Ala Ala Ala Asn Ser
 545 550 555 560

Arg Lys Pro Val Asn Lys Leu Leu
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<210> 20

<211> 1692

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1692)

<223>

<400> 20

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gtc aac gtt aac acc gtt ttc ggt ttg cca ggt gac ttc aac ttg tcc	96
Val Asn Val Asn Thr Val Phe Gly Leu Pro Gly Asp Phe Asn Leu Ser	
20 25 30	
ttg ttg gac aag atc tac gaa gtt gaa ggt atg aga tgg gct ggt aac	144
Leu Leu Asp Lys Ile Tyr Glu Val Glu Gly Met Arg Trp Ala Gly Asn	
35 40 45	
gcc aac gaa ttg aac gct gct tac gcc gct gat ggt tac gct cgt atc	192
Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ile	
50 55 60	
aag ggt atg tct tgt atc atc acc acc ttc ggt gtc ggt gaa ttg tct	240
Lys Gly Met Ser Cys Ile Ile Thr Thr Phe Gly Val Gly Glu Leu Ser	
65 70 75 80	
gct ttg aac ggt att gcc ggt tct tac gct gaa cac gtc ggt gtt ttg	288
Ala Leu Asn Gly Ile Ala Gly Ser Tyr Ala Glu His Val Gly Val Leu	
85 90 95	
cac gtt gtt ggt gtc cca tcc atc tct gct caa gct aag caa ttg ttg	336
His Val Val Gly Val Pro Ser Ile Ser Ala Gln Ala Lys Gln Leu Leu	
100 105 110	
ttg cac cac acc ttg ggt aac ggt gac ttc act gtt ttc cac aga atg	384
Leu His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met	
115 120 125	
tct gcc aac att tct gaa acc act gct atg atc act gac att gct acc	432
Ser Ala Asn Ile Ser Glu Thr Thr Ala Met Ile Thr Asp Ile Ala Thr	
130 135 140	
gcc cca gct gaa att gac aga tgt atc aga acc act tac gtc acc caa	480
Ala Pro Ala Glu Ile Asp Arg Cys Ile Arg Thr Thr Tyr Val Thr Gln	
145 150 155 160	
aga cca gtc tac tta ggt ttg cca gct aac ttg gtc gac ttg aac gtc	528
Arg Pro Val Tyr Leu Gly Leu Pro Ala Asn Leu Val Asp Leu Asn Val	
165 170 175	
cca gct aag ttg ttg caa act cca att gac atg tct ttg aag cca aac	576
Pro Ala Lys Leu Leu Gln Thr Pro Ile Asp Met Ser Leu Lys Pro Asn	
180 185 190	
gat gct gaa tcc gaa aag gaa gtc att gac acc atc ttg gct ttg gtc	624
Asp Ala Glu Ser Glu Lys Glu Val Ile Asp Thr Ile Leu Ala Leu Val	
195 200 205	
aag gat gct aag aac cca gtt atc ttg gct gat gct tgt tgt tcc aga	672

Lys	Asp	Ala	Lys	Asn	Pro	Val	Ile	Leu	Ala	Asp	Ala	Cys	Cys	Ser	Arg	
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cac	gac	gtc	aag	gct	gaa	act	aag	aag	ttg	att	gac	ttg	act	caa	ttc	720
His	Asp	Val	Lys	Ala	Glu	Thr	Lys	Lys	Leu	Ile	Asp	Leu	Thr	Gln	Phe	
225					230				235						240	
cca	gct	ttc	gtc	acc	cca	atg	ggt	aag	ggt	tcc	att	gac	gaa	caa	cac	768
Pro	Ala	Phe	Val	Thr	Pro	Met	Gly	Lys	Gly	Ser	Ile	Asp	Glu	Gln	His	
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cca	aga	tac	ggt	ggt	gtt	tac	gtc	ggt	acc	ttg	tcc	aag	cca	gaa	gtt	816
Pro	Arg	Tyr	Gly	Gly	Val	Tyr	Val	Gly	Thr	Leu	Ser	Lys	Pro	Glu	Val	
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aag	gaa	gcc	gtt	gaa	tct	gct	gac	ttg	att	ttg	tct	gtc	ggt	gct	ttg	864
Lys	Glu	Ala	Val	Glu	Ser	Ala	Asp	Leu	Ile	Leu	Ser	Val	Gly	Ala	Leu	
	275						280					285				
ttg	tct	gat	ttc	aac	acc	ggt	tct	ttc	tct	tac	tct	tac	aag	acc	aag	912
Leu	Ser	Asp	Phe	Asn	Thr	Gly	Ser	Phe	Ser	Tyr	Ser	Tyr	Lys	Thr	Lys	
	290					295						300				
aac	att	gtc	gaa	ttc	cac	tcc	gac	cac	atg	aag	atc	aga	aac	gcc	act	960
Asn	Ile	Val	Glu	Phe	His	Ser	Asp	His	Met	Lys	Ile	Arg	Asn	Ala	Thr	
305					310					315					320	
ttc	cca	ggt	gtc	caa	atg	aaa	ttc	gtt	ttg	caa	aag	ttg	ttg	acc	act	1008
Phe	Pro	Gly	Val	Gln	Met	Lys	Phe	Val	Leu	Gln	Lys	Leu	Leu	Thr	Thr	
				325					330					335		
att	gct	gac	gcc	gct	aag	ggt	tac	aag	cca	gtt	gct	gtc	cca	gct	aga	1056
Ile	Ala	Asp	Ala	Ala	Lys	Gly	Tyr	Lys	Pro	Val	Ala	Val	Pro	Ala	Arg	
			340					345					350			
act	cca	gct	aac	gct	gct	gtc	cca	gct	tct	acc	cca	ttg	aag	caa	gaa	1104
Thr	Pro	Ala	Asn	Ala	Ala	Val	Pro	Ala	Ser	Thr	Pro	Leu	Lys	Gln	Glu	
		355					360					365				
tgg	atg	tgg	aac	caa	ttg	ggt	aac	ttc	ttg	caa	gaa	ggt	gat	gtt	gtc	1152
Trp	Met	Trp	Asn	Gln	Leu	Gly	Asn	Phe	Leu	Gln	Glu	Gly	Asp	Val	Val	
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Ile	Ala	Glu	Thr	Gly	Thr	Ser	Ala	Phe	Gly	Ile	Asn	Gln	Thr	Thr	Phe	
385					390					395					400	
cca	aac	aac	acc	tac	ggt	atc	tct	caa	gtc	tta	tgg	ggt	tcc	att	ggt	1248
Pro	Asn	Asn	Thr	Tyr	Gly	Ile	Ser	Gln	Val	Leu	Trp	Gly	Ser	Ile	Gly	
				405					410					415		
ttc	acc	act	ggt	gct	acc	ttg	ggt	gct	gct	ttc	gct	gct	gaa	gaa	att	1296
Phe	Thr	Thr	Gly	Ala	Thr	Leu	Gly	Ala	Ala	Phe	Ala	Ala	Glu	Glu	Ile	
			420					425					430			
gat	cca	aag	aag	aga	gtt	atc	tta	ttc	att	ggt	gac	ggt	tct	ttg	caa	1344
Asp	Pro	Lys	Lys	Arg	Val	Ile	Leu	Phe	Ile	Gly	Asp	Gly	Ser	Leu	Gln	
		435					440					445				
ttg	act	gtt	caa	gaa	atc	tcc	acc	atg	atc	aga	tgg	ggc	ttg	aag	cca	1392

Leu Thr Val Gln Glu Ile Ser Thr Met Ile Arg Trp Gly Leu Lys Pro
 450 455 460
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 Tyr Leu Phe Val Leu Asn Asn Asp Gly Tyr Thr Ile Glu Lys Leu Ile
 465 470 475 480
 cac ggt cca aag gct caa tac aac gaa att caa ggt tgg gac cac cta 1488
 His Gly Pro Lys Ala Gln Tyr Asn Glu Ile Gln Gly Trp Asp His Leu
 485 490 495
 tcc ttg ttg cca act ttc ggt gct aag gac tat gaa acc cac aga gtc 1536
 Ser Leu Leu Pro Thr Phe Gly Ala Lys Asp Tyr Glu Thr His Arg Val
 500 505 510
 gct acc acc ggt gaa tgg gac aag ttg acc caa gac aag tct ttc aac 1584
 Ala Thr Thr Gly Glu Trp Asp Lys Leu Thr Gln Asp Lys Ser Phe Asn
 515 520 525
 gac aac tct aag atc aga atg att gaa atc atg ttg cca gtc ttc gat 1632
 Asp Asn Ser Lys Ile Arg Met Ile Glu Ile Met Leu Pro Val Phe Asp
 530 535 540
 gct cca caa aac ttg gtt gaa caa gct aag ttg act gct gct acc aac 1680
 Ala Pro Gln Asn Leu Val Glu Gln Ala Lys Leu Thr Ala Ala Thr Asn
 545 550 555 560
 gct aag caa taa 1692
 Ala Lys Gln

<210> 21

<211> 563

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 21

Met Ser Glu Ile Thr Leu Gly Lys Tyr Leu Phe Glu Arg Leu Lys Gln
 1 5 10 15
 Val Asn Val Asn Thr Val Phe Gly Leu Pro Gly Asp Phe Asn Leu Ser
 20 25 30
 Leu Leu Asp Lys Ile Tyr Glu Val Glu Gly Met Arg Trp Ala Gly Asn
 35 40 45
 Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ile
 50 55 60

Lys Gly Met Ser Cys Ile Ile Thr Thr Phe Gly Val Gly Glu Leu Ser
65 70 75 80

Ala Leu Asn Gly Ile Ala Gly Ser Tyr Ala Glu His Val Gly Val Leu
85 90 95

His Val Val Gly Val Pro Ser Ile Ser Ala Gln Ala Lys Gln Leu Leu
100 105 110

Leu His His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met
115 120 125

Ser Ala Asn Ile Ser Glu Thr Thr Ala Met Ile Thr Asp Ile Ala Thr
130 135 140

Ala Pro Ala Glu Ile Asp Arg Cys Ile Arg Thr Thr Tyr Val Thr Gln
145 150 155 160

Arg Pro Val Tyr Leu Gly Leu Pro Ala Asn Leu Val Asp Leu Asn Val
165 170 175

Pro Ala Lys Leu Leu Gln Thr Pro Ile Asp Met Ser Leu Lys Pro Asn
180 185 190

Asp Ala Glu Ser Glu Lys Glu Val Ile Asp Thr Ile Leu Ala Leu Val
195 200 205

Lys Asp Ala Lys Asn Pro Val Ile Leu Ala Asp Ala Cys Cys Ser Arg
210 215 220

His Asp Val Lys Ala Glu Thr Lys Lys Leu Ile Asp Leu Thr Gln Phe
225 230 235 240

Pro Ala Phe Val Thr Pro Met Gly Lys Gly Ser Ile Asp Glu Gln His
245 250 255

Pro Arg Tyr Gly Gly Val Tyr Val Gly Thr Leu Ser Lys Pro Glu Val
260 265 270

Lys Glu Ala Val Glu Ser Ala Asp Leu Ile Leu Ser Val Gly Ala Leu
275 280 285

Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser Tyr Lys Thr Lys
290 295 300

Asn Ile Val Glu Phe His Ser Asp His Met Lys Ile Arg Asn Ala Thr
 305 310 315 320

Phe Pro Gly Val Gln Met Lys Phe Val Leu Gln Lys Leu Leu Thr Thr
 325 330 335

Ile Ala Asp Ala Ala Lys Gly Tyr Lys Pro Val Ala Val Pro Ala Arg
 340 345 350

Thr Pro Ala Asn Ala Ala Val Pro Ala Ser Thr Pro Leu Lys Gln Glu
 355 360 365

Trp Met Trp Asn Gln Leu Gly Asn Phe Leu Gln Glu Gly Asp Val Val
 370 375 380

Ile Ala Glu Thr Gly Thr Ser Ala Phe Gly Ile Asn Gln Thr Thr Phe
 385 390 395 400

Pro Asn Asn Thr Tyr Gly Ile Ser Gln Val Leu Trp Gly Ser Ile Gly
 405 410 415

Phe Thr Thr Gly Ala Thr Leu Gly Ala Ala Phe Ala Ala Glu Glu Ile
 420 425 430

Asp Pro Lys Lys Arg Val Ile Leu Phe Ile Gly Asp Gly Ser Leu Gln
 435 440 445

Leu Thr Val Gln Glu Ile Ser Thr Met Ile Arg Trp Gly Leu Lys Pro
 450 455 460

Tyr Leu Phe Val Leu Asn Asn Asp Gly Tyr Thr Ile Glu Lys Leu Ile
 465 470 475 480

His Gly Pro Lys Ala Gln Tyr Asn Glu Ile Gln Gly Trp Asp His Leu
 485 490 495

Ser Leu Leu Pro Thr Phe Gly Ala Lys Asp Tyr Glu Thr His Arg Val
 500 505 510

Ala Thr Thr Gly Glu Trp Asp Lys Leu Thr Gln Asp Lys Ser Phe Asn
 515 520 525

Asp Asn Ser Lys Ile Arg Met Ile Glu Ile Met Leu Pro Val Phe Asp
 530 535 540

Ala Pro Gln Asn Leu Val Glu Gln Ala Lys Leu Thr Ala Ala Thr Asn
 545 550 555 560

Ala Lys Gln

<210> 22

<211> 33

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 22

tctttaatta atgggttgtc cgtcattcat ata

33

<210> 23

<211> 32

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 23

ctaaagcttt taggccagag tggtcttgcg cg

32

<210> 24

<211> 1674

<212> DNA

<213> Acetobacter pasteurianus

<220>

<221> CDS

<222> (1)..(1674)

<223>

<400> 24

gtg acc tat act gtt ggc atg tat ctt gca gaa cgc ctt gta cag atc	48
Val Thr Tyr Thr Val Gly Met Tyr Leu Ala Glu Arg Leu Val Gln Ile	
1 5 10 15	
ggg ctg aag cat cac ttc gcc gtg ggc ggc gac tac aat ctc gtt ctt	96
Gly Leu Lys His His Phe Ala Val Gly Gly Asp Tyr Asn Leu Val Leu	
20 25 30	
ctg gat cag ttg ctc ctc aac aag gac atg aaa cag atc tat tgc tgc	144
Leu Asp Gln Leu Leu Leu Asn Lys Asp Met Lys Gln Ile Tyr Cys Cys	
35 40 45	
aat gag ttg aac tgt ggc ttc agc gcg gaa ggc tac gcc cgt tct aac	192
Asn Glu Leu Asn Cys Gly Phe Ser Ala Glu Gly Tyr Ala Arg Ser Asn	
50 55 60	
ggg gct gcg gca gcg gtt gtc acc ttc agc gtt ggc gcc att tcc gcc	240
Gly Ala Ala Ala Ala Val Val Thr Phe Ser Val Gly Ala Ile Ser Ala	
65 70 75 80	
atg aac gcc ctc ggc ggc gcc tat gcc gaa aac ctg ccg gtt atc ctg	288
Met Asn Ala Leu Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu	
85 90 95	
att tcc ggc gcg ccc aac agc aat gat cag ggc aca ggt cat atc ctg	336
Ile Ser Gly Ala Pro Asn Ser Asn Asp Gln Gly Thr Gly His Ile Leu	
100 105 110	
cat cac aca atc ggc aag acg gat tac agc tac cag ctt gaa atg gcc	384
His His Thr Ile Gly Lys Thr Asp Tyr Ser Tyr Gln Leu Glu Met Ala	
115 120 125	
cgt cag gtc acc tgt gcc gcc gaa agc att acc gac gct cac tcc gcc	432
Arg Gln Val Thr Cys Ala Ala Glu Ser Ile Thr Asp Ala His Ser Ala	
130 135 140	
ccg gcc aag att gac cac gtc att cgc acg gcg ctg cgc gag cgt aag	480
Pro Ala Lys Ile Asp His Val Ile Arg Thr Ala Leu Arg Glu Arg Lys	
145 150 155 160	
ccg gcc tat ctg gac atc gcg tgc aac att gcc tcc gag ccc tgc gtg	528
Pro Ala Tyr Leu Asp Ile Ala Cys Asn Ile Ala Ser Glu Pro Cys Val	
165 170 175	
cgg cct ggc cct gtc agc agc ctg ctg tcc gag cct gaa atc gac cac	576
Arg Pro Gly Pro Val Ser Ser Leu Leu Ser Glu Pro Glu Ile Asp His	
180 185 190	
acg agc ctg aag gcc gca gtg gac gcc acg gtt gcc ttg ctg aaa aat	624
Thr Ser Leu Lys Ala Ala Val Asp Ala Thr Val Ala Leu Leu Lys Asn	
195 200 205	
cgg cca gcc ccc gtc atg ctg ctg ggc agc aag ctg cgg gcc gcc aac	672
Arg Pro Ala Pro Val Met Leu Leu Gly Ser Lys Leu Arg Ala Ala Asn	
210 215 220	

gca ctg gcc gca acc gaa acg ctg gca gac aag ctg caa tgc gcg gtg Ala Leu Ala Ala Thr Glu Thr Leu Ala Asp Lys Leu Gln Cys Ala Val 225 230 235 240	720
acc atc atg gcg gcc gcg aaa ggc ttt ttc ccc gaa gac cac gcg ggt Thr Ile Met Ala Ala Ala Lys Gly Phe Phe Pro Glu Asp His Ala Gly 245 250 255	768
ttc cgc ggc ctg tac tgg ggc gaa gtc tcg aac ccc ggc gtg cag gaa Phe Arg Gly Leu Tyr Trp Gly Glu Val Ser Asn Pro Gly Val Gln Glu 260 265 270	816
ctg gtg gag acc tcc gac gca ctg ctg tgc atc gcc ccc gta ttc aac Leu Val Glu Thr Ser Asp Ala Leu Leu Cys Ile Ala Pro Val Phe Asn 275 280 285	864
gac tat tca aca gtc ggc tgg tcg ggc atg ccc aag ggc ccc aat gtg Asp Tyr Ser Thr Val Gly Trp Ser Gly Met Pro Lys Gly Pro Asn Val 290 295 300	912
att ctg gct gag ccc gac cgc gta acg gtc gat ggc cgc gcc tat gac Ile Leu Ala Glu Pro Asp Arg Val Thr Val Asp Gly Arg Ala Tyr Asp 305 310 315 320	960
ggc ttt acc ctg cgc gcc ttc ctg cag gct ctg gcg gaa aaa gcc ccc Gly Phe Thr Leu Arg Ala Phe Leu Gln Ala Leu Ala Glu Lys Ala Pro 325 330 335	1008
gcg cgc ccg gcc tcc gca cag aaa agc agc gtc ccg acg tgc tcg ctc Ala Arg Pro Ala Ser Ala Gln Lys Ser Ser Val Pro Thr Cys Ser Leu 340 345 350	1056
acc gcg aca tcc gat gaa gcc ggt ctg acg aat gac gaa atc gtc cgt Thr Ala Thr Ser Asp Glu Ala Gly Leu Thr Asn Asp Glu Ile Val Arg 355 360 365	1104
cat atc aac gcc ctg ctg aca tca aac acg acg ctg gtg gca gaa acc His Ile Asn Ala Leu Leu Thr Ser Asn Thr Thr Leu Val Ala Glu Thr 370 375 380	1152
ggc gat tca tgg ttc aat gcc atg cgc atg acc ctg gcc ggt gcg cgc Gly Asp Ser Trp Phe Asn Ala Met Arg Met Thr Leu Ala Gly Ala Arg 385 390 395 400	1200
gtg gaa ctg gaa atg cag tgg ggc cat atc ggc tgg tcc gtg ccc tcc Val Glu Leu Glu Met Gln Trp Gly His Ile Gly Trp Ser Val Pro Ser 405 410 415	1248
gcg ttc ggc aat gcc atg ggc tcg cag gac cgc cag cat gtg gtg atg Ala Phe Gly Asn Ala Met Gly Ser Gln Asp Arg Gln His Val Val Met 420 425 430	1296
gta ggc gat ggc tcc ttc cag ctt acc gcg cag gaa gtg gct cag atg Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Val Ala Gln Met 435 440 445	1344
gtg cgc tac gaa ctg ccc gtc att atc ttt ctg atc aac aac cgt ggc Val Arg Tyr Glu Leu Pro Val Ile Ile Phe Leu Ile Asn Asn Arg Gly 450 455 460	1392

tat gtc att gaa atc gcc att cat gac ggc ccg tac aac tat atc aag 1440
 Tyr Val Ile Glu Ile Ala Ile His Asp Gly Pro Tyr Asn Tyr Ile Lys
 465 470 475 480

aac tgg gat tac gcc ggc ctg atg gaa gtc ttc aac gcc gga gaa ggc 1488
 Asn Trp Asp Tyr Ala Gly Leu Met Glu Val Phe Asn Ala Gly Glu Gly
 485 490 495

cat gga ctt ggc ctg aaa gcc acc acc ccg aag gaa ctg aca gaa gcc 1536
 His Gly Leu Gly Leu Lys Ala Thr Thr Pro Lys Glu Leu Thr Glu Ala
 500 505 510

atc gcc agg gca aaa gcc aat acc cgc ggc ccg acg ctg atc gaa tgc 1584
 Ile Ala Arg Ala Lys Ala Asn Thr Arg Gly Pro Thr Leu Ile Glu Cys
 515 520 525

cag atc gac cgc acg gac tgc acg gat atg ctg gtt caa tgg ggc cgc 1632
 Gln Ile Asp Arg Thr Asp Cys Thr Asp Met Leu Val Gln Trp Gly Arg
 530 535 540

aag gtt gcc tca acc aac gcg cgc aag acc act ctg gcc tga 1674
 Lys Val Ala Ser Thr Asn Ala Arg Lys Thr Thr Leu Ala
 545 550 555

<210> 25

<211> 557

<212> PRT

<213> *Acetobacter pasteurianus*

<400> 25

Val Thr Tyr Thr Val Gly Met Tyr Leu Ala Glu Arg Leu Val Gln Ile
 1 5 10 15

Gly Leu Lys His His Phe Ala Val Gly Gly Asp Tyr Asn Leu Val Leu
 20 25 30

Leu Asp Gln Leu Leu Leu Asn Lys Asp Met Lys Gln Ile Tyr Cys Cys
 35 40 45

Asn Glu Leu Asn Cys Gly Phe Ser Ala Glu Gly Tyr Ala Arg Ser Asn
 50 55 60

Gly Ala Ala Ala Ala Val Val Thr Phe Ser Val Gly Ala Ile Ser Ala
 65 70 75 80

Met Asn Ala Leu Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu
 85 90 95

Ile Ser Gly Ala Pro Asn Ser Asn Asp Gln Gly Thr Gly His Ile Leu
 100 105 110

His His Thr Ile Gly Lys Thr Asp Tyr Ser Tyr Gln Leu Glu Met Ala
 115 120 125

Arg Gln Val Thr Cys Ala Ala Glu Ser Ile Thr Asp Ala His Ser Ala
 130 135 140

Pro Ala Lys Ile Asp His Val Ile Arg Thr Ala Leu Arg Glu Arg Lys
 145 150 155 160

Pro Ala Tyr Leu Asp Ile Ala Cys Asn Ile Ala Ser Glu Pro Cys Val
 165 170 175

Arg Pro Gly Pro Val Ser Ser Leu Leu Ser Glu Pro Glu Ile Asp His
 180 185 190

Thr Ser Leu Lys Ala Ala Val Asp Ala Thr Val Ala Leu Leu Lys Asn
 195 200 205

Arg Pro Ala Pro Val Met Leu Leu Gly Ser Lys Leu Arg Ala Ala Asn
 210 215 220

Ala Leu Ala Ala Thr Glu Thr Leu Ala Asp Lys Leu Gln Cys Ala Val
 225 230 235 240

Thr Ile Met Ala Ala Ala Lys Gly Phe Phe Pro Glu Asp His Ala Gly
 245 250 255

Phe Arg Gly Leu Tyr Trp Gly Glu Val Ser Asn Pro Gly Val Gln Glu
 260 265 270

Leu Val Glu Thr Ser Asp Ala Leu Leu Cys Ile Ala Pro Val Phe Asn
 275 280 285

Asp Tyr Ser Thr Val Gly Trp Ser Gly Met Pro Lys Gly Pro Asn Val
 290 295 300

Ile Leu Ala Glu Pro Asp Arg Val Thr Val Asp Gly Arg Ala Tyr Asp
 305 310 315 320

Gly Phe Thr Leu Arg Ala Phe Leu Gln Ala Leu Ala Glu Lys Ala Pro
 325 330 335

Ala Arg Pro Ala Ser Ala Gln Lys Ser Ser Val Pro Thr Cys Ser Leu
 340 345 350

Thr Ala Thr Ser Asp Glu Ala Gly Leu Thr Asn Asp Glu Ile Val Arg
 355 360 365

His Ile Asn Ala Leu Leu Thr Ser Asn Thr Thr Leu Val Ala Glu Thr
 370 375 380

Gly Asp Ser Trp Phe Asn Ala Met Arg Met Thr Leu Ala Gly Ala Arg
 385 390 395 400

Val Glu Leu Glu Met Gln Trp Gly His Ile Gly Trp Ser Val Pro Ser
 405 410 415

Ala Phe Gly Asn Ala Met Gly Ser Gln Asp Arg Gln His Val Val Met
 420 425 430

Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Val Ala Gln Met
 435 440 445

Val Arg Tyr Glu Leu Pro Val Ile Ile Phe Leu Ile Asn Asn Arg Gly
 450 455 460

Tyr Val Ile Glu Ile Ala Ile His Asp Gly Pro Tyr Asn Tyr Ile Lys
 465 470 475 480

Asn Trp Asp Tyr Ala Gly Leu Met Glu Val Phe Asn Ala Gly Glu Gly
 485 490 495

His Gly Leu Gly Leu Lys Ala Thr Thr Pro Lys Glu Leu Thr Glu Ala
 500 505 510

Ile Ala Arg Ala Lys Ala Asn Thr Arg Gly Pro Thr Leu Ile Glu Cys
 515 520 525

Gln Ile Asp Arg Thr Asp Cys Thr Asp Met Leu Val Gln Trp Gly Arg
 530 535 540

Lys Val Ala Ser Thr Asn Ala Arg Lys Thr Thr Leu Ala
 545 550 555

<211> 32

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 26

atcttaatta atgtataccg ttggtatgta ct

32

<210> 27

<211> 34

<212> DNA

<213> artificial sequence

<220>

<223> artificial sequence

<400> 27

tatgcggccg cttacgcttg tggtttgcca gagt

34

<210> 28

<211> 1671

<212> DNA

<213> Zymobacter palmae

<220>

<221> CDS

<222> (1)..(1671)

<223>

<400> 28

atg tat acc gtt ggt atg tac ttg gca gaa cgc cta gcc cag atc ggc
Met Tyr Thr Val Gly Met Tyr Leu Ala Glu Arg Leu Ala Gln Ile Gly
1 5 10 15

48

ctg aaa cac cac ttt gcc gtg gcc ggt gac tac aac ctg gtg ttg ctt

96

Leu	Lys	His	His	Phe	Ala	Val	Ala	Gly	Asp	Tyr	Asn	Leu	Val	Leu	Leu	
			20					25					30			
gat	cag	ctc	ctg	ctg	aac	aaa	gac	atg	gag	cag	gtc	tac	tgc	tgt	aac	144
Asp	Gln	Leu	Leu	Leu	Asn	Lys	Asp	Met	Glu	Gln	Val	Tyr	Cys	Cys	Asn	
		35					40					45				
gaa	ctt	aac	tgc	ggc	ttt	agc	gcc	gaa	ggc	tac	gct	cgt	gca	cgt	ggc	192
Glu	Leu	Asn	Cys	Gly	Phe	Ser	Ala	Glu	Gly	Tyr	Ala	Arg	Ala	Arg	Gly	
	50					55					60					
gcc	gcc	gct	gcc	atc	gtc	acg	ttc	agc	gta	ggc	gct	atc	tct	gca	atg	240
Ala	Ala	Ala	Ala	Ile	Val	Thr	Phe	Ser	Val	Gly	Ala	Ile	Ser	Ala	Met	
65					70					75					80	
aac	gcc	atc	ggc	ggc	gcc	tat	gca	gaa	aac	ctg	ccg	gtc	atc	ctg	atc	288
Asn	Ala	Ile	Gly	Gly	Ala	Tyr	Ala	Glu	Asn	Leu	Pro	Val	Ile	Leu	Ile	
			85						90					95		
tct	ggc	tca	ccg	aac	acc	aat	gac	tac	ggc	aca	ggc	cac	atc	ctg	cac	336
Ser	Gly	Ser	Pro	Asn	Thr	Asn	Asp	Tyr	Gly	Thr	Gly	His	Ile	Leu	His	
			100					105					110			
cac	acc	att	ggc	act	act	gac	tat	aac	tat	cag	ctg	gaa	atg	gta	aaa	384
His	Thr	Ile	Gly	Thr	Thr	Asp	Tyr	Asn	Tyr	Gln	Leu	Glu	Met	Val	Lys	
		115					120					125				
cac	gtt	acc	tgc	gca	cgt	gaa	agc	atc	gtt	tct	gcc	gaa	gaa	gca	ccg	432
His	Val	Thr	Cys	Ala	Arg	Glu	Ser	Ile	Val	Ser	Ala	Glu	Glu	Ala	Pro	
	130					135					140					
gca	aaa	atc	gac	cac	gtc	atc	cgt	acg	gct	cta	cgt	gaa	cgc	aaa	ccg	480
Ala	Lys	Ile	Asp	His	Val	Ile	Arg	Thr	Ala	Leu	Arg	Glu	Arg	Lys	Pro	
145					150					155					160	
gct	tat	ctg	gaa	atc	gca	tgc	aac	gtc	gct	ggc	gct	gaa	tgt	gtt	cgt	528
Ala	Tyr	Leu	Glu	Ile	Ala	Cys	Asn	Val	Ala	Gly	Ala	Glu	Cys	Val	Arg	
			165					170						175		
ccg	ggc	ccg	atc	aat	agc	ctg	ctg	cgt	gaa	ctc	gaa	gtt	gac	cag	acc	576
Pro	Gly	Pro	Ile	Asn	Ser	Leu	Leu	Arg	Glu	Leu	Glu	Val	Asp	Gln	Thr	
			180					185					190			
agt	gtc	act	gcc	gct	gta	gat	gcc	gcc	gta	gaa	tggt	ctg	cag	gac	cgc	624
Ser	Val	Thr	Ala	Ala	Val	Asp	Ala	Ala	Val	Glu	Trp	Leu	Gln	Asp	Arg	
		195					200					205				
cag	aac	gtc	gtc	atg	ctg	gtc	ggc	agc	aaa	ctg	cgt	gcc	gct	gcc	gct	672
Gln	Asn	Val	Val	Met	Leu	Val	Gly	Ser	Lys	Leu	Arg	Ala	Ala	Ala	Ala	
	210					215					220					
gaa	aaa	cag	gct	gtt	gcc	cta	gcg	gac	cgc	ctg	ggc	tgc	gct	gtc	acg	720
Glu	Lys	Gln	Ala	Val	Ala	Leu	Ala	Asp	Arg	Leu	Gly	Cys	Ala	Val	Thr	
225					230					235				240		
atc	atg	gct	gcc	gaa	aaa	ggc	ttc	ttc	ccg	gaa	gat	cat	ccg	aac	ttc	768
Ile	Met	Ala	Ala	Glu	Lys	Gly	Phe	Phe	Pro	Glu	Asp	His	Pro	Asn	Phe	
			245						250					255		
cgc	ggc	ctg	tac	tgg	ggc	gaa	gtc	agc	tcc	gaa	ggc	gca	cag	gaa	ctg	816

Arg	Gly	Leu	Tyr	Trp	Gly	Glu	Val	Ser	Ser	Glu	Gly	Ala	Gln	Glu	Leu	
			260					265					270			
gtt	gaa	aac	gcc	gat	gcc	atc	ctg	tgt	ctg	gca	ccg	gta	ttc	aac	gac	864
Val	Glu	Asn	Ala	Asp	Ala	Ile	Leu	Cys	Leu	Ala	Pro	Val	Phe	Asn	Asp	
		275					280					285				
tat	gct	acc	gtt	ggc	tgg	aac	tcc	tgg	ccg	aaa	ggc	gac	aat	gtc	atg	912
Tyr	Ala	Thr	Val	Gly	Trp	Asn	Ser	Trp	Pro	Lys	Gly	Asp	Asn	Val	Met	
	290					295					300					
gtc	atg	gac	acc	gac	cgc	gtc	act	ttc	gca	gga	cag	tcc	ttc	gaa	ggc	960
Val	Met	Asp	Thr	Asp	Arg	Val	Thr	Phe	Ala	Gly	Gln	Ser	Phe	Glu	Gly	
305					310					315					320	
ctg	tca	ttg	agc	acc	ttc	gcc	gca	gca	ctg	gct	gag	aaa	gca	cct	tct	1008
Leu	Ser	Leu	Ser	Thr	Phe	Ala	Ala	Ala	Leu	Ala	Glu	Lys	Ala	Pro	Ser	
			325						330					335		
cgc	ccg	gca	acg	act	caa	ggc	act	caa	gca	ccg	gta	ctg	ggc	att	gag	1056
Arg	Pro	Ala	Thr	Thr	Gln	Gly	Thr	Gln	Ala	Pro	Val	Leu	Gly	Ile	Glu	
		340					345						350			
gcc	gca	gag	ccc	aat	gca	ccg	ctg	acc	aat	gac	gaa	atg	acg	cgt	cag	1104
Ala	Ala	Glu	Pro	Asn	Ala	Pro	Leu	Thr	Asn	Asp	Glu	Met	Thr	Arg	Gln	
		355					360					365				
atc	cag	tcg	ctg	atc	act	tcc	gac	act	act	ctg	aca	gca	gaa	aca	ggc	1152
Ile	Gln	Ser	Leu	Ile	Thr	Ser	Asp	Thr	Thr	Leu	Thr	Ala	Glu	Thr	Gly	
	370					375					380					
gac	tct	tgg	ttc	aac	gct	tct	cgc	atg	ccg	att	cct	ggc	ggc	gct	cgt	1200
Asp	Ser	Trp	Phe	Asn	Ala	Ser	Arg	Met	Pro	Ile	Pro	Gly	Gly	Ala	Arg	
385					390					395					400	
gtc	gaa	ctg	gaa	atg	caa	tgg	ggc	cat	atc	ggc	tgg	tcc	gta	cct	tct	1248
Val	Glu	Leu	Glu	Met	Gln	Trp	Gly	His	Ile	Gly	Trp	Ser	Val	Pro	Ser	
			405						410					415		
gca	ttc	ggc	aac	gcc	gtt	ggc	tct	ccg	gag	cgt	cgc	cac	atc	atg	atg	1296
Ala	Phe	Gly	Asn	Ala	Val	Gly	Ser	Pro	Glu	Arg	Arg	His	Ile	Met	Met	
		420					425						430			
gtc	ggc	gat	ggc	tct	ttc	cag	ctg	act	gct	caa	gaa	gtt	gct	cag	atg	1344
Val	Gly	Asp	Gly	Ser	Phe	Gln	Leu	Thr	Ala	Gln	Glu	Val	Ala	Gln	Met	
		435					440					445				
atc	cgc	tat	gaa	atc	ccg	gtc	atc	atc	ttc	ctg	atc	aac	aac	cgc	ggc	1392
Ile	Arg	Tyr	Glu	Ile	Pro	Val	Ile	Ile	Phe	Leu	Ile	Asn	Asn	Arg	Gly	
	450					455					460					
tac	gtc	atc	gaa	atc	gct	atc	cat	gac	ggc	cct	tac	aac	tac	atc	aaa	1440
Tyr	Val	Ile	Glu	Ile	Ala	Ile	His	Asp	Gly	Pro	Tyr	Asn	Tyr	Ile	Lys	
465					470					475					480	
aac	tgg	aac	tac	gct	ggc	ctg	atc	gac	gtc	ttc	aat	gac	gaa	gat	ggc	1488
Asn	Trp	Asn	Tyr	Ala	Gly	Leu	Ile	Asp	Val	Phe	Asn	Asp	Glu	Asp	Gly	
			485						490					495		
cat	ggc	ctg	ggc	ctg	aaa	gct	tct	act	ggc	gca	gaa	cta	gaa	ggc	gct	1536

His Gly Leu Gly Leu Lys Ala Ser Thr Gly Ala Glu Leu Glu Gly Ala
 500 505 510

atc aag aaa gca ctc gac aat cgt cgc ggt ccg acg ctg atc gaa tgt 1584
 Ile Lys Lys Ala Leu Asp Asn Arg Arg Gly Pro Thr Leu Ile Glu Cys
 515 520 525

aac atc gct cag gac gac tgc act gaa acc ctg att gct tgg ggt aaa 1632
 Asn Ile Ala Gln Asp Asp Cys Thr Glu Thr Leu Ile Ala Trp Gly Lys
 530 535 540

cgt gta gca gct acc aac tct cgc aaa cca caa gcg taa 1671
 Arg Val Ala Ala Thr Asn Ser Arg Lys Pro Gln Ala
 545 550 555

<210> 29

<211> 556

<212> PRT

<213> Zymobacter palmae

<400> 29

Met Tyr Thr Val Gly Met Tyr Leu Ala Glu Arg Leu Ala Gln Ile Gly
 1 5 10 15

Leu Lys His His Phe Ala Val Ala Gly Asp Tyr Asn Leu Val Leu Leu
 20 25 30

Asp Gln Leu Leu Leu Asn Lys Asp Met Glu Gln Val Tyr Cys Cys Asn
 35 40 45

Glu Leu Asn Cys Gly Phe Ser Ala Glu Gly Tyr Ala Arg Ala Arg Gly
 50 55 60

Ala Ala Ala Ala Ile Val Thr Phe Ser Val Gly Ala Ile Ser Ala Met
 65 70 75 80

Asn Ala Ile Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu Ile
 85 90 95

Ser Gly Ser Pro Asn Thr Asn Asp Tyr Gly Thr Gly His Ile Leu His
 100 105 110

His Thr Ile Gly Thr Thr Asp Tyr Asn Tyr Gln Leu Glu Met Val Lys
 115 120 125

His Val Thr Cys Ala Arg Glu Ser Ile Val Ser Ala Glu Glu Ala Pro
 130 135 140

Ala Lys Ile Asp His Val Ile Arg Thr Ala Leu Arg Glu Arg Lys Pro
 145 150 155 160

Ala Tyr Leu Glu Ile Ala Cys Asn Val Ala Gly Ala Glu Cys Val Arg
 165 170 175

Pro Gly Pro Ile Asn Ser Leu Leu Arg Glu Leu Glu Val Asp Gln Thr
 180 185 190

Ser Val Thr Ala Ala Val Asp Ala Ala Val Glu Trp Leu Gln Asp Arg
 195 200 205

Gln Asn Val Val Met Leu Val Gly Ser Lys Leu Arg Ala Ala Ala Ala
 210 215 220

Glu Lys Gln Ala Val Ala Leu Ala Asp Arg Leu Gly Cys Ala Val Thr
 225 230 235 240

Ile Met Ala Ala Glu Lys Gly Phe Phe Pro Glu Asp His Pro Asn Phe
 245 250 255

Arg Gly Leu Tyr Trp Gly Glu Val Ser Ser Glu Gly Ala Gln Glu Leu
 260 265 270

Val Glu Asn Ala Asp Ala Ile Leu Cys Leu Ala Pro Val Phe Asn Asp
 275 280 285

Tyr Ala Thr Val Gly Trp Asn Ser Trp Pro Lys Gly Asp Asn Val Met
 290 295 300

Val Met Asp Thr Asp Arg Val Thr Phe Ala Gly Gln Ser Phe Glu Gly
 305 310 315 320

Leu Ser Leu Ser Thr Phe Ala Ala Ala Leu Ala Glu Lys Ala Pro Ser
 325 330 335

Arg Pro Ala Thr Thr Gln Gly Thr Gln Ala Pro Val Leu Gly Ile Glu
 340 345 350

Ala Ala Glu Pro Asn Ala Pro Leu Thr Asn Asp Glu Met Thr Arg Gln
 355 360 365

Ile Gln Ser Leu Ile Thr Ser Asp Thr Thr Leu Thr Ala Glu Thr Gly
 370 375 380

Asp Ser Trp Phe Asn Ala Ser Arg Met Pro Ile Pro Gly Gly Ala Arg
 385 390 395 400

Val Glu Leu Glu Met Gln Trp Gly His Ile Gly Trp Ser Val Pro Ser
 405 410 415

Ala Phe Gly Asn Ala Val Gly Ser Pro Glu Arg Arg His Ile Met Met
 420 425 430

Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln Glu Val Ala Gln Met
 435 440 445

Ile Arg Tyr Glu Ile Pro Val Ile Ile Phe Leu Ile Asn Asn Arg Gly
 450 455 460

Tyr Val Ile Glu Ile Ala Ile His Asp Gly Pro Tyr Asn Tyr Ile Lys
 465 470 475 480

Asn Trp Asn Tyr Ala Gly Leu Ile Asp Val Phe Asn Asp Glu Asp Gly
 485 490 495

His Gly Leu Gly Leu Lys Ala Ser Thr Gly Ala Glu Leu Glu Gly Ala
 500 505 510

Ile Lys Lys Ala Leu Asp Asn Arg Arg Gly Pro Thr Leu Ile Glu Cys
 515 520 525

Asn Ile Ala Gln Asp Asp Cys Thr Glu Thr Leu Ile Ala Trp Gly Lys
 530 535 540

Arg Val Ala Ala Thr Asn Ser Arg Lys Pro Gln Ala
 545 550 555

<210> 30

<211> 32

<212> DNA

<213> artificial sequence

<400> 30

ctattaatta atggcttcgg tacacggcac ca

<210> 31

<211> 34

<212> . DNA

<213> artificial sequence

<400> 31

tatgcggccg cttacttcac cgggcttacg gtgc

34

<210> 32

<211> 1587

<212> DNA

<213> Pseudomonas putida

 $\langle 220 \rangle$

<221> CDS

<222> (1) .. (1584)

<223>

<400> 32

atg gct tgc gta cac ggc acc aca tac gaa ctc ttg cga cgt caa ggc 48
Met Ala Ser Val His Gly Thr Thr Tyr Glu Leu Leu Arg Arg Gln Gly
1 5 10 15

atc gat acg gtc ttc ggc aat cct ggc tog aac gag ctc cgg ttt ttg 96
Ile Asp Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
20 25 30

aag gac ttt cca gag gac ttt cga tac atc ctg gct ttg cag gaa gcg 144
Lys Asp Phe Pro Glu Asp Phe Arg Tyr Ile Leu Ala Leu Gln Glu Ala
35 40 45

tgt gtg gtg ggc att gca gac ggc tat gcg caa gcc agt cgg aag ccg 192
Cys Val Val Gly Ile Ala Asp Gly Tyr Ala Gln Ala Ser Arg Lys Pro
50 55 60

gct ttc att aac ctg cat tct gct gct ggt acc ggc aat gct atg ggt 240
Ala Phe Ile Asn Leu His Ser Ala Ala Gly Thr Gly Asn Ala Met Gly
65 70 75 80

gca ctc agt aac gcc tgg aac tca cat tcc ccg ctg atc gtc act gcc 288
Ala Leu Ser Asn Ala Trp Asn Ser His Ser Pro Leu Ile Val Thr Ala
85 90 95

ggc cag cag acc agg gcg atg att ggc gtt gaa gct ctg ctg acc aac Gly Gln Gln Thr Arg Ala Met Ile Gly Val Glu Ala Leu Leu Thr Asn 100 105 110	336
gtc gat gcc gcc aac ctg cca cga cca ctt gtc aaa tgg agc tac gag Val Asp Ala Ala Asn Leu Pro Arg Pro Leu Val Lys Trp Ser Tyr Glu 115 120 125	384
ccc gca agc gca gca gaa gtc cct cat gcg atg agc agg gct atc cat Pro Ala Ser Ala Ala Glu Val Pro His Ala Met Ser Arg Ala Ile His 130 135 140	432
atg gca agc atg gcg cca caa ggc cct gtc tat ctt tcg gtg cca tat Met Ala Ser Met Ala Pro Gln Gly Pro Val Tyr Leu Ser Val Pro Tyr 145 150 155 160	480
gac gat tgg gat aag gat gct gat cct cag tcc cac cac ctt ttt gat Asp Asp Trp Asp Lys Asp Ala Asp Pro Gln Ser His His Leu Phe Asp 165 170 175	528
cgc cat gtc agt tca tca gta cgc ctg aac gac cag gat ctc gat att Arg His Val Ser Ser Ser Val Arg Leu Asn Asp Gln Asp Leu Asp Ile 180 185 190	576
ctg gtg aaa gct ctc aac agc gca tcc aac ccg gcg atc gtc ctg ggc Leu Val Lys Ala Leu Asn Ser Ala Ser Asn Pro Ala Ile Val Leu Gly 195 200 205	624
ccg gac gtc gac gca gca aat gcg aac gca gac tgc gtc atg ttg gcc Pro Asp Val Asp Ala Ala Asn Ala Asn Ala Asp Cys Val Met Leu Ala 210 215 220	672
gaa cgc ctc aaa gct ccg gtt tgg gtt gcg cca tcc gct cca cgc tgc Glu Arg Leu Lys Ala Pro Val Trp Val Ala Pro Ser Ala Pro Arg Cys 225 230 235 240	720
cca ttc cct acc cgt cat cct tgc ttc cgt gga ttg atg cca gct ggc Pro Phe Pro Thr Arg His Pro Cys Phe Arg Gly Leu Met Pro Ala Gly 245 250 255	768
atc gca gcg att tct cag ctg ctc gaa ggt cac gat gtg gtt ttg gta Ile Ala Ala Ile Ser Gln Leu Leu Glu Gly His Asp Val Val Leu Val 260 265 270	816
atc ggc gct cca gtg ttc cgt tac cac caa tac gac cca ggt caa tat Ile Gly Ala Pro Val Phe Arg Tyr His Gln Tyr Asp Pro Gly Gln Tyr 275 280 285	864
ctc aaa cct ggc acg cga ttg att tcg gtg acc tgc gac ccg ctc gaa Leu Lys Pro Gly Thr Arg Leu Ile Ser Val Thr Cys Asp Pro Leu Glu 290 295 300	912
gct gca cgc gcg cca atg ggc gat gcg atc gtg gca gac att ggt gcg Ala Ala Arg Ala Pro Met Gly Asp Ala Ile Val Ala Asp Ile Gly Ala 305 310 315 320	960
atg gct agc gct ctt gcc aac ttg gtt gaa gag agc agc cgc cag ctc Met Ala Ser Ala Leu Ala Asn Leu Val Glu Glu Ser Ser Arg Gln Leu 325 330 335	1008

cca act gca gct ccg gaa ccc gcg aag gtt gac caa gac gct ggc cga Pro Thr Ala Ala Pro Glu Pro Ala Lys Val Asp Gln Asp Ala Gly Arg 340 345 350	1056
ctt cac cca gag aca gtg ttc gac aca ctg aac gac atg gcc ccg gag Leu His Pro Glu Thr Val Phe Asp Thr Leu Asn Asp Met Ala Pro Glu 355 360 365	1104
aat gcg att tac ctg aac gag tcg act tca acg acc gcc caa atg tgg Asn Ala Ile Tyr Leu Asn Glu Ser Thr Ser Thr Thr Ala Gln Met Trp 370 375 380	1152
cag cgc ctg aac atg cgc aac cct ggt agc tac tac ttc tgt gca gct Gln Arg Leu Asn Met Arg Asn Pro Gly Ser Tyr Tyr Phe Cys Ala Ala 385 390 395 400	1200
ggc gga ctg ggc ttc gcc ctg cct gca gca att ggc gtt caa ctc gca Gly Gly Leu Gly Phe Ala Leu Pro Ala Ala Ile Gly Val Gln Leu Ala 405 410 415	1248
gaa ccc gag cga caa gtc atc gcc gtc att ggc gac gga tcg gcg aac Glu Pro Glu Arg Gln Val Ile Ala Val Ile Gly Asp Gly Ser Ala Asn 420 425 430	1296
tac agc att agt gcg ttg tgg act gca gct cag tac aac atc ccc act Tyr Ser Ile Ser Ala Leu Trp Thr Ala Ala Gln Tyr Asn Ile Pro Thr 435 440 445	1344
atc ttc gtg atc atg aac aac ggc acc tac ggt gcg ttg cga tgg ttt Ile Phe Val Ile Met Asn Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe 450 455 460	1392
gcc ggc gtt ctc gaa gca gaa aac gtt cct ggg ctg gat gtg cca ggg Ala Gly Val Leu Glu Ala Glu Asn Val Pro Gly Leu Asp Val Pro Gly 465 470 475 480	1440
atc gac ttc cgc gca ctc gcc aag ggc tat ggt gtc caa gcg ctg aaa Ile Asp Phe Arg Ala Leu Ala Lys Gly Tyr Gly Val Gln Ala Leu Lys 485 490 495	1488
gcc gac aac ctt gag cag ctc aag ggt tcg cta caa gaa gcg ctt tct Ala Asp Asn Leu Glu Gln Leu Lys Gly Ser Leu Gln Glu Ala Leu Ser 500 505 510	1536
gcc aaa ggc ccg gta ctt atc gaa gta agc acc gta agc ccg gtg aag Ala Lys Gly Pro Val Leu Ile Glu Val Ser Thr Val Ser Pro Val Lys 515 520 525	1584
tga	1587

<210> 33

<211> 528

<212> PRT

<213> Pseudomonas putida

<400> 33

Met Ala Ser Val His Gly Thr Thr Tyr Glu Leu Leu Arg Arg Gln Gly
 1 5 10 15

Ile Asp Thr Val Phe Gly Asn Pro Gly Ser Asn Glu Leu Pro Phe Leu
 20 25 30

Lys Asp Phe Pro Glu Asp Phe Arg Tyr Ile Leu Ala Leu Gln Glu Ala
 35 40 45

Cys Val Val Gly Ile Ala Asp Gly Tyr Ala Gln Ala Ser Arg Lys Pro
 50 55 60

Ala Phe Ile Asn Leu His Ser Ala Ala Gly Thr Gly Asn Ala Met Gly
 65 70 75 80

Ala Leu Ser Asn Ala Trp Asn Ser His Ser Pro Leu Ile Val Thr Ala
 85 90 95

Gly Gln Gln Thr Arg Ala Met Ile Gly Val Glu Ala Leu Leu Thr Asn
 100 105 110

Val Asp Ala Ala Asn Leu Pro Arg Pro Leu Val Lys Trp Ser Tyr Glu
 115 120 125

Pro Ala Ser Ala Ala Glu Val Pro His Ala Met Ser Arg Ala Ile His
 130 135 140

Met Ala Ser Met Ala Pro Gln Gly Pro Val Tyr Leu Ser Val Pro Tyr
 145 150 155 160

Asp Asp Trp Asp Lys Asp Ala Asp Pro Gln Ser His His Leu Phe Asp
 165 170 175

Arg His Val Ser Ser Ser Val Arg Leu Asn Asp Gln Asp Leu Asp Ile
 180 185 190

Leu Val Lys Ala Leu Asn Ser Ala Ser Asn Pro Ala Ile Val Leu Gly
 195 200 205

Pro Asp Val Asp Ala Ala Asn Ala Asn Ala Asp Cys Val Met Leu Ala
 210 215 220

Glu Arg Leu Lys Ala Pro Val Trp Val Ala Pro Ser Ala Pro Arg Cys
 225 230 235 240
 Pro Phe Pro Thr Arg His Pro Cys Phe Arg Gly Leu Met Pro Ala Gly
 245 250 255
 Ile Ala Ala Ile Ser Gln Leu Leu Glu Gly His Asp Val Val Leu Val
 260 265 270
 Ile Gly Ala Pro Val Phe Arg Tyr His Gln Tyr Asp Pro Gly Gln Tyr
 275 280 285
 Leu Lys Pro Gly Thr Arg Leu Ile Ser Val Thr Cys Asp Pro Leu Glu
 290 295 300
 Ala Ala Arg Ala Pro Met Gly Asp Ala Ile Val Ala Asp Ile Gly Ala
 305 310 315 320
 Met Ala Ser Ala Leu Ala Asn Leu Val Glu Glu Ser Ser Arg Gln Leu
 325 330 335
 Pro Thr Ala Ala Pro Glu Pro Ala Lys Val Asp Gln Asp Ala Gly Arg
 340 345 350
 Leu His Pro Glu Thr Val Phe Asp Thr Leu Asn Asp Met Ala Pro Glu
 355 360 365
 Asn Ala Ile Tyr Leu Asn Glu Ser Thr Ser Thr Thr Ala Gln Met Trp
 370 375 380
 Gln Arg Leu Asn Met Arg Asn Pro Gly Ser Tyr Tyr Phe Cys Ala Ala
 385 390 395 400
 Gly Gly Leu Gly Phe Ala Leu Pro Ala Ala Ile Gly Val Gln Leu Ala
 405 410 415
 Glu Pro Glu Arg Gln Val Ile Ala Val Ile Gly Asp Gly Ser Ala Asn
 420 425 430
 Tyr Ser Ile Ser Ala Leu Trp Thr Ala Ala Gln Tyr Asn Ile Pro Thr
 435 440 445
 Ile Phe Val Ile Met Asn Asn Gly Thr Tyr Gly Ala Leu Arg Trp Phe
 450 455 460

Ala Gly Val Leu Glu Ala Glu Asn Val Pro Gly Leu Asp Val Pro Gly
465 470 475 480

Ile Asp Phe Arg Ala Leu Ala Lys Gly Tyr Gly Val Gln Ala Leu Lys
485 490 495

Ala Asp Asn Leu Glu Gln Leu Lys Gly Ser Leu Gln Glu Ala Leu Ser
500 505 510

Ala Lys Gly Pro Val Leu Ile Glu Val Ser Thr Val Ser Pro Val Lys
515 520 525